WHAT IS CLAIMED IS:

1. A peptide of the formula R^1-Asp-Lys-Gly-X-Y-Leu-Pro-Arg-Pro-Thr-Pro-Pro-Arg-Pro-Ile-Tyr-X'-Y'-R^2 SEQ ID NO:1, wherein said Thr is not glycosylated,

wherein R^1 is a moiety having a net positive charge other than L-Val;

wherein R^2 is selected from the group consisting of a free hydroxyl, an amide, an imide, a sugar, and a sequence of one or up to about 15 additional amino acids, optionally substituted with a free hydroxyl, an amide, an imide or a sugar, said additional amino acids being independently selected from L-configuration or D-configuration and said additional amino acids capable of cyclizing the peptide by bridging between the N- and C- termini thereof;

wherein X and Y form a dipeptide selected from the group consisting of Ser-Tyr and a dipeptide formed of naturally occurring amino acids or unnatural amino acids, said dipeptide resistant to cleavage; and

wherein X' and Y' form a dipeptide selected from the group consisting of Asn-Arg, and a dipeptide formed of naturally occurring amino acids or unnatural amino acids, said dipeptide resistant to cleavage.

2. The peptide according to claim 1, wherein R^1 is selected from the group consisting of

(a) a straight chain, branched, cyclic or heterocyclic alkyl group,

(b) a straight chain, branched, cyclic or heterocyclic alkanoyl group,

(c) a positively charged reporter group; and

(d) between 1 to 15 additional amino acids independently selected from L-configuration or D-configuration; said additional amino acids optionally substituted by one or more of (a), (b) or (c), and said additional amino acids capable of cyclizing the peptide by bridging between the N- and C- termini thereof.

3. The peptide according to claim 2, wherein said R^1 group (d) are amino acids which have been cyclized by the insertion into the structure of the amino acid of modifying sugars or imide.

4. The peptide according to claim 2, wherein said R^1 group (a) is 1-aminocyclo-hexane carboxylic acid.

5. The peptide according to claim 2, wherein said R^1 group (d) is selected from the additional amino acid residues D-Val-, Arg-Val-, Lys-Val-, Lys-Val-Asp-Lys-Val-, and -Arg-Pro-Pro-Thr-Pro-Arg-Pro-Leu-Lys-Val-.

6. The peptide according to claim 1, wherein said R^1 group is selected from Acetyl-Arg-Val-; Acetyl-Lys-Val-; and Acetyl-Lys-Val-Asp-Lys-Val-.

7. The peptide according to claim 2, wherein said R^1 group (c) is biotin.

8. The peptide according to claim 2 wherein said R^1 group provides a detectable signal, optionally upon interaction with other compounds.

9. The peptide according to claim 8 wherein said R^1 group (c) is 5(6) carboxyfluorescein.

10. The peptide according to claim 2 wherein R^1 group (c) is radioactive.

11. The peptide according to claim 2 wherein R^1 group (d) is a spacer interposed between the N- terminus and C- terminus of said peptide, permitting cyclization of said peptide.

39. The peptide according to claim 1 wherein at least one conventional amide bond between two amino acids in said sequence is replaced with a non-cleavable bond.

40. The peptide according to claim 39, wherein said non-cleavable bond is a thio-amide bond or a reduced amide bond.

41. A composition comprising multiple peptides of the formula R^1-Asp-Lys-Gly-X-Y-Leu-Pro-Arg-Pro-Thr-Pro-Pro-Arg-Pro-Ile-Tyr-X'-Y'-R^2 SEQ ID NO: 1,

wherein R^1 is a moiety having a net positive charge;

wherein R^2 is selected from the group consisting of:

(a) a free hydroxyl, an amide, an imide, or a sugar;

(b) a sequence of one or up to about 5 additional naturally occurring or unnatural amino acids, optionally substituted with a free hydroxyl, an amide, an imide or a sugar,

(c) a sequence of (b) wherein said additional amino acids cyclize the peptide by bridging between the N- and C- termini thereof; and

(d) a sequence of (b), wherein said additional amino acids link at least two said peptides;

wherein X and Y form a dipeptide selected from the group consisting of Ser-Tyr and a dipeptide formed of naturally occurring amino acids or unnatural amino acids, said dipeptide resistant to cleavage,

wherein X' and Y' form a dipeptide selected from the group consisting of Asn-Arg, and a dipeptide formed of naturally occurring amino acids or unnatural amino acids, said dipeptide resistant to cleavage.

42. The composition according to claim 41, comprising at least two peptides, wherein the second peptide is attached to any amino acid of the first peptide.

43. The composition according to claim 42, wherein additional peptides are attached to any amino acid of the other peptides in the composition.

44. The composition according to claim 41, comprising at least two said peptides, wherein at least one or more of said peptides is attached to a carrier.

45. The composition according to claim 41, comprising at least two peptides of claim 1, wherein the second or additional peptides is attached to a branched construct of the other peptides in the composition.

46. The composition according to claim 41, comprising at least two peptides of claim 1, wherein each additional peptide is covalently linked to R^2 of another peptide in the composition.

47. The composition according to claim 41, which is a multiple antigenic peptide.

48. The composition according to claim 47, wherein said multiple antigenic peptide comprises a β-alanine substituent on a poly-lysine core.

49. The composition according to claim 47, comprising at least four peptides.

72. A compound produced or identified by the method of claim 68 or 69.

73. The peptide according to claim 1, which is fused to a second protein.

74. A composition according to claim 41, wherein R^2 of one said peptide is a β-acetyl-2,3- diamino propionic acid group and wherein an additional said peptide is linked to the same R^2 at the carboxyl terminus.

75. A peptide of the formula R^1-Asp-Lys-Gly-X-Y-Leu-Pro-Arg-Pro-Thr-Pro-Pro-Arg-Pro-Ile-Tyr-X'-Y'-R^2 SEQ ID NO:1, wherein said Thr is not glycosylated,

wherein R^1 is a moiety having a net positive charge;

wherein R^2 is selected from the group consisting of a free hydroxyl, an amide, an imide, a sugar, and a sequence of one or up to about 15 additional amino acids, optionally substituted with a free hydroxyl, an amide, an imide or a sugar, said additional amino acids being independently selected from L-configuration or D-configuration and said additional amino acids capable of cyclizing the peptide by bridging between the N- and C- termini thereof;

wherein X and Y form a dipeptide selected from the group consisting of Ser-Tyr and a dipeptide formed of naturally occurring amino acids or unnatural amino acids, said dipeptide resistant to cleavage; and

wherein X' and Y' form a dipeptide selected from the group consisting of Asn-Arg, and a dipeptide formed of naturally occurring amino acids or unnatural amino acids, said dipeptide resistant to cleavage.